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5'-TACGGACAGAACT-3' (SEQ ID NO:1), both located from position 582 to 595 as referred to the wild type human hepatitis B virus genome. These modifications include a fluorescent dye, 6-(fluorescein-6-carboxamido) hexanoate (6FAM), at its 5' terminus and a primary amine group at its 3' terminus. The resulting oligonucleotides that are immobilized on solid glass supports have the following structure: 5'-(6FAM)TACGGACGGAACTGTTTTTTTTTTTTT (C-7 amine)-3' (SEQ ID NO:4), and 5'-(6FAM)TACGGACAGAACTGTTTTTTTTTTTTT (C-7 amine)-3' (SEQ ID NO:5), and the second oligonucleotide contains the mutation G to A (position 8) leading to change at amino acid 145 (Glycine to Arginine) of human hepatitis B virus surface antigen. There is also an inclusion of a poly-T (underlined) as a synthetic linker aiming at facilitating the subsequent hybridization reaction with target human viral DNA sequences from serum samples.--

Please replace the paragraph starting at page 14, line 31 with the following rewritten paragraph:

--As a direct application of the novel detection system in the present invention, modifications have been added to two oligonucleotides (listed herein): 5'-TACGGACGGAACT-3' (SEQ ID NO:3), and 5'-TACGGACAGAACT-3'' (SEQ ID NO:1), both located from position 582 to 595 as referred to the wild type human hepatitis B virus genome. These include a fluorescent dye, 6-(fluorescein-6-carboxamido) hexanoate, at its 5' terminus for microscopic detection and a primary amine group at its 3' terminus allowing its immobilization on solid glass supports. The resulting oligonucleotides that are immobilized on solid glass supports has the following structure: 5'-(6FAM)TACGGACGGAACTGTTTTTTTTTTTTT